

## **Impact of Measurement Errors on Predicting Pork Carcass Composition: Within Sample Evaluation**

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Regression equations for estimating fat-free lean mass are widely used in the pork industry to predict carcass composition, carcass value and nutrient requirements. These prediction equations are used to evaluate the differences between pigs of different genetic populations, sexes and experimental treatments. However, most prediction equations currently in use have not been evaluated for the extent to which they account for genetic population and sex differences.

Two opinions exist to the best method to develop prediction equations. One opinion is that in the development of the prediction equations, carcass measurements should be collected by a commercial pork processor. The optical probe or carcass ultrasound measurements should be taken under the same conditions as the prediction equations are to be used. The second opinion, based on statistical theory, is that the carcass measurements should be taken carefully in a laboratory setting to minimize measurement errors. The objective of this study was to use simulation to examine the impact of measurement errors on the ability of commonly used prediction equations to accurately predict genetic population and sex differences in fat-free lean mass.

### **Materials and Methods**

A program was written to simulate the relationships between carcass fat-free lean mass (FFLM, lbs) and carcass measurements. Carcass weight (CW, lbs), fat depth (FD, in.), and muscle depth (MD, in.) were simulated. The means and correlations of the simulated traits were based on previous research data (Hicks et al., 1998), and are shown in Table 1. Fat-free lean mass was calculated as:

$$\text{FFLM} = 10.23 + (.459 \times \text{CW}) - (24.7 \times \text{FD}) + (6.55 \times \text{MD}) + e_{ij}$$

where  $e_{ij}$  was a random error assigned to each pig (mean=0, SD=4.7 lbs). A large data set was simulated containing 900 genetic populations. These genetic populations were divided into 9 groups based on their means for FD and MD (1/3 above average, 1/3 average, and 1/3 below average for each trait). Subsets of the data were created by randomly selecting one genetic population from each of the nine groups. Fifty subsets of nine genetic populations with 16 pigs/sex in each population (total n=288) were randomly chosen for analysis. Measurement errors for FD and MD were simulated for each pig, which reduced the relationship (correlation) of each variable with FFLM by 15, 30, and 45% from the values without measurement errors (0%). Based on previous research, the random measurement errors for FD and MD were simulated to have correlations of -.50.

Equations to predict FFLM from CW, FD, and MD were derived for each subset and level of measurement error. The  $R^2$  and residual standard deviation (RSD) of the prediction equations were evaluated. The correlation of the true and predicted genetic population means and the variance ratio (the variance of the predicted genetic population means divided by the variance

of the true genetic population means) were evaluated as measures of genetic population biases. The ability of each equation to predict the actual sex difference was also evaluated.

## Results

As the level of simulated measurement errors increased, the  $R^2$  of the prediction equations decreased, residual standard deviation increased, and regression coefficients for CW, MD and FD decreased in absolute value (Table 2). The regression coefficient for muscle depth was affected to the greatest extent, as the “b” values for muscle depth with the largest magnitude of errors was only 32% as large as the “b” value with no measurement errors. The regression coefficient for carcass weight was affected the least.

The prediction equations were less able to detect true differences between genetic populations and sexes as measurement errors increased (Table 3). Variance ratios, an indicator of the percent of true variation between the nine genetic populations predicted by the equations, were near 1.0 with no measurement errors, and decreased to .55, .32 and .20 as measurement errors increased. The correlations between the predicted and actual genetic population means for fat-free lean decreased as measurement errors increased. Also, the prediction equations predicted a smaller difference between barrows and gilts as the measurement errors increased.

## Implications

All prediction equations should be carefully evaluated as to the magnitude of sub-population (genetic population, sex or treatment) biases. Pork producers and animal scientists should not use prediction equations to evaluate genetic populations, sexes or experimental treatments unless the carcass measurements used in the development of the prediction equation were accurately collected. Data used in the development of prediction equations must be collected as accurately as possible.

## Reference

Hicks, C., A.P. Schinckel, J.C. Forrest, J.T. Akridge, J.R. Wagner, and W. Chen. 1998. Biases associated with genotype and sex in prediction of fat-free lean mass and carcass value in hogs. J. Anim. Sci. 76:2221-2234.

Table 1. Means and correlations of the carcass measurements and fat-free lean.

| Variable           | Mean  | Barrows | Gilts | S.D. | Correlation |      |      |
|--------------------|-------|---------|-------|------|-------------|------|------|
|                    |       |         |       |      | FD          | MD   | FFLM |
| Carcass Weight, lb | 185.2 | 185.2   | 185.2 | 22.1 | .30         | .20  | .70  |
| Fat Depth, in.     | .98   | 1.12    | .85   | .28  |             | -.30 | -.35 |
| Muscle Depth, in.  | 1.96  | 1.85    | 2.06  | .21  |             |      | .45  |
| Fat-Free Lean, lb  | 83.7  | 79.8    | 87.7  | 5.43 |             |      |      |

Table 2. Regression coefficient and measurement error level.

| Measurement<br>Error Level <sup>a</sup> | R <sup>2</sup> | RSD, lb | b values <sup>b</sup> |                |                |                |
|---|----------------|---------|-----------------------|----------------|----------------|----------------|
|   |                |         | b <sub>0</sub>        | b <sub>1</sub> | b <sub>2</sub> | b <sub>3</sub> |
| 0%                                      | .843           | 4.42    | 10.97                 | .459           | -24.8          | 6.20           |
| 15%                                     | .735           | 6.11    | 15.12                 | .434           | -20.5          | 4.27           |
| 30%                                     | .652           | 7.01    | 17.48                 | .415           | -16.5          | 2.93           |
| 45%                                     | .589           | 7.63    | 18.41                 | .400           | -12.7          | 1.99           |

<sup>a</sup> The simulation was conducted such that as the level of measurement errors increased, the correlation of muscle depth (MD) and fat depth (FD) with FFLM were reduced to 15, 30 or 45% from the values with no measurement errors (0%).

<sup>b</sup> The equations are fat-free lean mass (lbs) = b<sub>0</sub> + b<sub>1</sub> (carcass weight, lbs) + b<sub>2</sub> (fat depth, in.) + b<sub>3</sub> (muscle depth, in.).

Table 3. Summary statistics<sup>a</sup> describing the magnitude of genetic population and sex differences.

| Measurement<br>Error Level | CR  | VR   | % Sex Difference |
|----------------------------|-----|------|------------------|
| 0%                         | .98 | 1.00 | 98.9             |
| 15%                        | .95 | .55  | 68.8             |
| 30%                        | .88 | .32  | 46.2             |
| 45%                        | .76 | .20  | 29.5             |

<sup>a</sup> CR = correlation of the true and predicted genetic population means; VR = variance of the predicted genetic population means divided by true variation of the genetic populations; % sex difference = the predicted difference between the barrows and gilts divided by the true difference.